

INPUT SET: S2395.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

wrapped
text

SEQUENCE LISTING

2
3 (1) General Information:
4
5 (i) APPLICANTS: *Start response on this line*
6 ↑ Hauptmann, R.
7 Falkner, E.
8 Bodo, G.
9 VoÃ, T.
10 Maurer- Fogy, I.
11
12 (ii) TITLE OF INVENTION: Process for Preparing and Purifying
13 alpha-Interferon
14
15 (iii) NUMBER OF SEQUENCES: 12
16
17 (iv) CORRESPONDENCE ADDRESS:
18 (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox
19 (B) STREET: 1100 New York Avenue, Suite 600
20 (C) CITY: Washington
21 (D) STATE: D.C.
22 (E) COUNTRY: U.S.A.
23 (F) ZIP: 20005
24
25 (v) COMPUTER READABLE FORM:
26 (A) MEDIUM TYPE: Floppy disk
27 (B) COMPUTER: IBM PC compatible
28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
30
31 (vi) CURRENT APPLICATION DATA:
32 (A) APPLICATION NUMBER:
33 (B) FILING DATE: herewith
34 (C) CLASSIFICATION:
35 *deke space* *Information:*
36 (vii) ATTORNEY/AGENT NUMBER:
37 (A) NAME: Esmond, Robert W. RWE/EG
38 (B) REGISTRATION NUMBER: 32,893
39 (C) REFERENCE/DOCKET NUMBER: 0652.1350000
40
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: (202) 371-2600
43 (B) TELEFAX: (202) 371-2540
44
45

INPUT SET: S2395.raw

46

ERRORED SEQUENCES FOLLOW:

61 (2) INFORMATION FOR SEQ ID NO: 2:
62
63 (i) SEQUENCE CHARACTERISTICS:
--> 64 (A) LENGTH: 56 base pairs
65 (B) TYPE: nucleic acid
66 (C) STRANDEDNESS: both
67 (D) TOPOLOGY: unknown
68
69 (ii) MOLECULE TYPE: cDNA
70
71
72
73 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
74
75 GACTTCAGAA GCTTCTGCAG TTACGATCGT TATCATTCCCT TACCTTCTTAA ACTTTC
76 56
77

56

156 (2) INFORMATION FOR SEQ ID NO: 6:
157
158 (i) SEQUENCE CHARACTERISTICS:
--> 159 (A) LENGTH: 495 base pairs
160 (B) TYPE: nucleic acid
161 (C) STRANDEDNESS: both
162 (D) TOPOLOGY: unknown
163
164 (ii) MOLECULE TYPE: cDNA
165
166
167 (ix) FEATURE:
168 (A) NAME/KEY: CDS
169 (B) LOCATION: 1..495
170
171
172 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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174 TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG AGG ACC TTG ATG
175
176 48
177 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
178 1 5 10 15
179
180 CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC TGC TTG AAG GAC
181
182 96
183 Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp

48

etc

↓

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671DATE: 06/16/94
TIME: 10:49:13

INPUT SET: S2395.raw

184 20 25 30
185
186 AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC AAC CAG TTC CAA
187
188 144
189 Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
190 35 40 45
191
192 AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC CAG CAG ATC TTC
193
194 192
195 Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
196 50 55 60
197
198 AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG GAT GAG ACC CTC
199
200 240
201 Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
202 65 70 75 80
203
204 CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG AAT GAC CTG GAA
205
206 288
207 Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
208 85 90 95
209
210 GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT CCC CTG ATG AAG
211
212 336
213 Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
214 100 105 110
215
216 GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA AGA ATC ACT CTC
217
218 384
219 Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
220 115 120 125
221
222 TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG GAG GTT GTC AGA
223
224 432
225 Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
226 130 135 140
227
228 GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC TTG CAA GAA AGT
229
230 480
231 Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
232 145 150 155 160
233
234 TTA AGA AGT AAG GAA
235 495
236 Leu Arg Ser Lys Glu

INPUT SET: S2395.raw

237 165
238
239

284 (2) INFORMATION FOR SEQ ID NO: 8:

285
286 (i) SEQUENCE CHARACTERISTICS:
--> 287 (A) LENGTH: 869 base pairs
288 (B) TYPE: nucleic acid
289 (C) STRANDEDNESS: both
290 (D) TOPOLOGY: unknown
291292 (ii) MOLECULE TYPE: cDNA
293
294
295

296 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

297
298 GAATTCTGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA
--> 299 CCAACAGCGG 60
300
301 TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAGC CCGATGCCAG
302 CATTCCCTGAC
303 120
304
305 GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC
306 TCGTCAGTAA
307 180
308
309 AAAGTTAACATC TTTTCAACAG CTGTCATAAA GTTGTACCGG CCGAGACTTA
310 TAGTCGCTTT
311 240
312
313 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA
314 AAAGAATATC
315 300
316
317 GCATTCTTC TTGCATCTAT GTTCGTTTT TCTATTGCTA CAAATGCCTA
318 TGCATGTGAT
319 360
320
321 CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC
322 ACAGATGAGG
323 420
324
325 AGAATCTCTC TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTCC
326 CCAGGAGGAG
327 480
328
329 TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT
330 GATCCAGCAG
331 540
332

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671DATE: 06/16/94
TIME: 10:49:30

INPUT SET: S2395.raw

333 ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCTT GGGATGAGAC
334 CCTCCTAGAC
335 600
336
337 AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTGG AAGCCTGTGT
338 GATACAGGGG
339 660
340
341 GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT
342 GAGGAAATAC
343 720
344
345 TTCCAAAGAA TCAC TCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC
346 CTGGGAGGTT
347 780
348
349 GTCAGAGCAG AAATCATGAG ATCTTTTCT TTGTCAACAA ACTTGCAAGA
350 AAGTTTAAGA
351 840
352
353 AGTAAGGAAT GATAACGATC GTAATGCA
354 869
355

356 (2) INFORMATION FOR SEQ ID NO: 9:

357

358 (i) SEQUENCE CHARACTERISTICS:

--> 359 (A) LENGTH: 1177 base pairs
360 (B) TYPE: nucleic acid
361 (C) STRANDEDNESS: both
362 (D) TOPOLOGY: unknown
363

364 (ii) MOLECULE TYPE: cDNA
365

366

367 (ix) FEATURE:

368 (A) NAME/KEY: CDS
369 (B) LOCATION: 286..873
370 (D) OTHER INFORMATION: /function= "Cytokine"
371 /product= "Interferon-omegal"
372

373 (ix) FEATURE:

374 (A) NAME/KEY: mat_peptide
375 (B) LOCATION: 355..873
376 (D) OTHER INFORMATION: /function= "Cytokine"
377 /product= "Interferon-omega"
378

379 (ix) FEATURE:

380 (A) NAME/KEY: sig_peptide
381 (B) LOCATION: 286..354
382 (D) OTHER INFORMATION: /product= "ST II Leader"
383
384

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671DATE: 06/16/94
TIME: 10:49:39

INPUT SET: S2395.raw

385 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
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387 GAATGGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA
388 CCAACAGCGG
389 60
390
391 TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG
392 CATTCCCTGAC
393 120
394
395 GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC
396 TCGTCAGTAA
397 180
398
399 AAAGTTAACATC TTTTCAACAG CTGTCATAAA GTTGTACCGG CCGAGACTTA
400 TAGTCGCTTT
401 240
402
403 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTT ATG AAA AAG
404
405 294
406 Met Lys Lys
407 -23
408
409 AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ATT GCT ACA
410 342
411 Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala Thr
412 -20 -15 -10 -5
413
414 AAT GCC TAT GCA TGT GAT CTG CCT CAG AAC CAT GGC CTA CTT AGC AGG
415
416 390
417 Asn Ala Tyr Ala Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg
418 1 5 10
419
420 AAC ACC TTG GTG CTT CTG CAC CAA ATG AGG AGA ATC TCC CCT TTC TTG
421
422 438
423 Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu
424 15 20 25
425
426 TGT CTC AAG GAC AGA AGA GAC TTC AGG TTC CCC CAG GAG ATG GTA AAA
427
428 486
429 Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val Lys
430 30 35 40
431
432 GGG AGC CAG TTG CAG AAG GCC CAT GTC ATG TCT GTC CTC CAT GAG ATG
433
434 534
435 Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu His Glu Met
436 45 50 55 60
437

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671DATE: 06/16/94
TIME: 10:49:48

INPUT SET: S2395.raw

438 CTG CAG CAG ATC TTC AGC CTC TTC CAC ACA GAG CGC TCC TCT GCT GCC
439
440 582
441 Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala
442 65 70 75
443
444 TGG AAC ATG ACC CTC CTA GAC CAA CTC CAC ACT GGA CTT CAT CAG CAA
445
446 630
447 Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu His Gln Gln
448 80 85 90
449
450 CTG CAA CAC CTG GAG ACC TGC TTG CTG CAG GTA GTG GGA GAA GGA GAA
451
452 678
453 Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly Glu Gly Glu
454 95 100 105
455
456 TCT GCT GGG GCA ATT AGC AGC CCT GCA CTG ACC TTG AGG AGG TAC TTC
457
458 726
459 Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe
460 110 115 120
461
462 CAG GGA ATC CGT GTC TAC CTG AAA GAG AAG AAA TAC AGC GAC TGT GCC
463
464 774
465 Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala
466 125 130 135 140
467
468 TGG GAA GTT GTC AGA ATG GAA ATC ATG AAA TCC TTG TTC TTA TCA ACA
469
470 822
471 Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr
472 145 150 155
473
474 AAC ATG CAA GAA AGA CTG AGA AGT AAA GAT AGA GAC CTG GGC TCA TCT
475
476 870
477 Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu Gly Ser Ser
478 160 165 170
479
480 TGAAATGATT CTCATTGATT AATTGCCAT ATAACACTTG CACATGTGAC
481 TCTGGTCAAT
482 930
483
484 TCAAAAGACT CTTATTCGG CTTAACAC AGAATTGACT GAATTAGTTC
485 TGCAAATACT
486 990
487
488 TTGTCGGTAT ATTAAGCCAG TATATGTTAA AAAGACTTAG GTTCAGGGGC
489 ATCAGTCCCT
490 1050

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671DATE: 06/16/94
TIME: 10:49:57

INPUT SET: S2395.raw

491 AAGATGTTAT TTATTTTAC TCATTTATTT ATTCTTACAT TTTATCATAT
492 TTATACTATT
493 1110
494
495 TATATTCTTA TATAACAAAT GTTGCCTTT ACATTGTATT AAGATAACAA
496 AACATGTTCA
497 1170
498
499 GGATCCA
500 1177
501
502

553 (2) INFORMATION FOR SEQ ID NO: 11:

554
555 (i) SEQUENCE CHARACTERISTICS:
556 (A) LENGTH: 879 base pairs
557 (B) TYPE: nucleic acid
558 (C) STRANDEDNESS: both
559 (D) TOPOLOGY: unknown
560

561 (ii) MOLECULE TYPE: cDNA
562
563
564

565 (ix) FEATURE:
566 (A) NAME/KEY: CDS
567 (B) LOCATION: 286..852
568
569 (ix) FEATURE:
570 (A) NAME/KEY: mat_peptide
571 (B) LOCATION: 355..852
572 (D) OTHER INFORMATION: /function= "Cytokine"
573 /product= "Interferon-alpha-2c"
574

575 (ix) FEATURE:
576 (A) NAME/KEY: sig_peptide
577 (B) LOCATION: 286..354
578 (D) OTHER INFORMATION: /product= "ST II Leader"
579
580

581 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

582
583 GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA
584 CCAACAGCGG
585 60
586
587 TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAGC CCGATGCCAG
588 CATTCTGAC
589 120
590
591 GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC
592 TCGTCAGTAA

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671DATE: 06/16/94
TIME: 10:50:05

INPUT SET: S2395.raw

593 180
594
595 AAAGTTAACATC TTTTCAACAG CTGTCATAAA GTTGTACGG CCGAGACTTA
596 TAGTCGCTTT
597 240
598
599 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTT ATG AAA AAG
600
601 294
602 Met Lys Lys
603 -23
604
605 AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ATT GCT ACA
606 342
607 Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala Thr
608 -20 -15 -10 -5
609
610 AAT GCC TAT GCA TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG
611
612 390
613 Asn Ala Tyr Ala Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg
614 1 5 10
615
616 AGG ACC TTG ATG CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC
617
618 438
619 Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser
620 15 20 25
621
622 TGC TTG AAG GAC AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC
623
624 486
625 Cys Leu Lys Asp Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly
626 30 35 40
627
628 AAC CAG TTC CAA AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC
629
630 534
631 Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile
632 45 50 55 60
633
634 CAG CAG ATC TTC AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG
635
636 582
637 Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp
638 65 70 75
639
640 GAT GAG ACC CTC CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG
641
642 630
643 Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu
644 80 85 90
645

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671DATE: 06/16/94
TIME: 10:50:14

INPUT SET: S2395.raw

646 AAT GAC CTG GAA GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT
647
648 678
649 Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr
650 95 100 105
651
652 CCC CTG ATG AAG GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA
653
654 726
655 Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln
656 110 115 120
657
658 AGA ATC ACT CTC TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG
659
660 774
661 Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp
662 125 130 135 140
663
664 GAG GTT GTC AGA GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC
665
666 822
667 Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn
668 145 150 155
669
670 TTG CAA GAA AGT TTA AGA AGT AAG GAA TGATAACGAT CGTAACTGCA
671
672 869
673 Leu Gln Glu Ser Leu Arg Ser Lys Glu
674 160 165
675
676 GAAGCTTAAT
677 879
678

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/249,671DATE: 06/16/94
TIME: 10:50:20

INPUT SET: S2395.raw

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANTS:
36	Unknown or Misplaced Identifier	(viii) ATTORNEY/ AGENT NUMBER:
37	Unknown or Misplaced Identifier	(A) NAME: Esmond, Robert W. RWE/EG
38	Unknown or Misplaced Identifier	(B) REGISTRATION NUMBER: 32,893
39	Unknown or Misplaced Identifier	(C) REFERENCE/DOCKET NUMBER: 0652.1350000
64	Entered (56) and Calc. Seq. Length (0) differ	(A) LENGTH: 56 base pairs
159	Entered (495) and Calc. Seq. Length (0) differ	(A) LENGTH: 495 base pairs
287	Entered (869) and Calc. Seq. Length (10) differ	(A) LENGTH: 869 base pairs
299	# of Sequences for line conflicts w/ running total	CCAACAGCGG 60
359	Entered (1177) and Calc. Seq. Length (0) differ	(A) LENGTH: 1177 base pairs
556	Entered (879) and Calc. Seq. Length (0) differ	(A) LENGTH: 879 base pairs